

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: May 7, 2003, 15:14:59 ; Search time 43 Seconds  
(without alignments)

6273.536 Million cell updates/sec

Title: US-09-965-830-1\_COPY\_6\_3257

Perfect score: 6089

Sequence: 1 atgcgcgcacatcgagcgcct.....aagaagcagcagggctctga 3252

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_n2p.model -DEV=xip  
-O=/cgn2\_1/USPTO.spool/US09965830/rnat\_07052003\_151448\_6247/app\_query.fasta.1.3399  
-DB=SwissProt\_40 -OPMT=fastan -SUFFIX=trp -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR.SCORE=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-USER=US09965830.ecgn\_1\_1\_70.grnat\_07052003\_151448\_6247 -NCPU=6 -ICPU=3  
-NO\_XIPXY -NO\_MAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV-TIMEOUT=120  
-WARN-TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1551	25.5	1159	1	HERG_HUMAN
2	1390	22.8	1174	1	CTKE_DROME
3	439	7.2	706	1	CNG3_BOVIN
4	429.5	7.1	683	1	CNG1_RAT
5	424.5	7.0	694	1	CNG3_HUMAN
6	423.5	7.0	735	1	CNG1_CHICK
7	422.5	6.9	631	1	CNG3_MOUSE
8	421.5	6.9	665	1	CNG_DROME
9	421.5	6.9	681	1	CNG1_CANFA
10	419	6.9	684	1	CNG1_MOUSE
11	414.5	6.8	682	1	CNG_ICPUP
12	413.5	6.8	690	1	CNG1_BOVIN
13	412	6.8	686	1	CNG1_HUMAN
14	411	6.7	645	1	CNG3_CHICK
15	405	6.7	664	1	CNG2_HUMAN
16	397.5	6.5	1464	1	CNG2_RABIT
17	395	6.5	664	1	CNG2_MOUSE
18	393	6.5	664	1	CNG2_RAT

## ALIGNMENTS

RESULT 1	HERG_HUMAN	STANDARD	PRT: 1159 AA.
AC	012809; 075680;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Voltage-gated potassium channel HerG (potassium channel, voltage-gated subfamily H member 2) (Ether-a-go-go-related protein).		
GN	KCNH2 OR HERG.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Hippocampus;		
RA	MEDLINE=94211879; PubMed=8159766;		
RA	Wanke J.W., Ganetzky B.;		
RT	"A family of potassium channel genes related to eag in Drosophila and mammals."		
RT	Proc. Natl. Acad. Sci. U.S.A. 91:3438-3442(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A., AND VARIANT IQT2 CYS-534.		
RA	MEDLINE=98260867; PubMed=9600240;		
RA	Itou T., Tanaka T., Nagai R., Kamiya T., Sawayama T., Nakayama T.,		
RA	Tomokke H., Sakurada H., Yazaki Y., Nakamura Y.;		
RT	"Genomic organization and mutational analysis of HERG, a gene responsible for familial long QT syndrome."		
RT	Hum. Genet. 102:435-439(1998).		
RN	[3]		
RP	SEQUENCE OF 27-1159 FROM N.A.		
RA	Yang P., Paulussen A., Verhaselt P., Crabbe R., Luyten W.,		
RA	Armstrong M.;		
RT	"Analysis of the human HERG gene: Intron localisation and identification of a novel inherited mutation associated with long QT."		
RT	Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.		
RL	[4]		
RP	VARIANTS IQT2 ASP-470; VAL-561; SER-628 AND 500-TLE--PHE-508 DEL.		
RX	MEDLINE=95196272; PubMed=7889573;		
RA	Curran M.E., Splawski I., Timothy K.W., Vincent G.M., Green E.D.,		

RT Keating M.T.;  
RA "A molecular basis for cardiac arrhythmia: HERG mutations cause long  
RT QT syndrome.";  
RT Cell 80:795-803(1995).  
RN [5]  
RN VARIANT LQT2 MET-822.  
RP MEDLINE-9625954; PubMed-8914737;  
RX Saitler C.A., Walsh E.P., Vesely M.R., Plummer M.H., Ginsburg G.S.,  
RA Jacob H.J.;  
RT "Novel missense mutation in the cyclic nucleotide-binding domain of  
RT HERG causes long QT syndrome.";  
RT Am. J. Med. Genet. 65:27-35(1996).  
RN [6]  
RN VARIANT LQT2 ARG-593.  
RP MEDLINE-9625954; PubMed-8635257;  
RX Benson D.W., Macrae C.A., Vesely M.R., Walsh E.P., Seidman J.G.,  
RA Seidman C.E., Saitler C.A.;  
RT "Missense mutation in the pore region of HERG causes familial long QT  
RT syndrome.";  
RT Circulation 93:1791-1795(1996).  
RN [7]  
RN VARIANTS LQT2 ILE-474; VAL-561; HIS-611; VAL-614 AND ALA-630.  
RX MEDLINE-9717660; PubMed-9024139;  
RA Tanaka T., Nagai R., Tomoike H., Takata S., Yano K., Yabuta K.,  
RA Hanada N., Nakano O., Shibata A., Sawayama T., Kasai H., Yazaki Y.,  
RA Nakamura Y.;  
RT "Four novel KVLQT1 and four novel HERG mutations in familial long-QT  
RT syndrome.";  
RT Circulation 95:565-567(1997).  
RN [8]  
RN VARIANTS LQT2 CYS-572; ASP-588; VAL-614 AND ALA-630.  
RX MEDLINE-98360095; PubMed-9693036;  
RA Splawski I., Shen J., Timothy K.W., Vincent G.M., Lehmann M.H.,  
RA Keating M.T.;  
RT "Genomic structure of three long QT syndrome genes: KVLQT1, HERG, and  
RT KCNE1.";  
RT Genomics 51:86-97(1998).  
RN [9]  
RN VARIANTS LQT2 LEU-612; VAL-614; ASP-629; SER-629 AND SER-633.  
RX MEDLINE-98204397; PubMed-9544837;  
RA Saitler C.A., Vesely M.R., Duggal P., Ginsburg G.S., Beggs A.H.;  
RT "Multiple different missense mutations in the pore region of HERG in  
RT patients with long QT syndrome.";  
RT Hum. Genet. 102:265-272(1998).  
RN [10]  
RN VARIANTS LQT2 SER-601.  
RX MEDLINE-98112459; PubMed-9452080;  
RA Akimoto K., Furutani M., Imamura S.-I., Furutani Y., Kasanuki H.,  
RA Takao A., Momma K., Matsuoaka R.;  
RT "Novel missense mutation (G601S) of HERG in a Japanese long QT  
RT syndrome family.";  
RT Hum. Mutat. Suppl. 1:S184-S186(1998).  
RN [11]  
RN VARIANTS LQT2 PRO-558; CYS-582; SER-604; MET-613 AND LEU-640.  
RX MEDLINE-99235550; PubMed-10220144;  
RA Jongblond R.J.E., Walde A.A.M., Geelen J.L.M.C., Doevendans P.,  
RA Schap C., Van Langen I., Van Tintelen J.P., Cobben J.M.,  
RA Beaufort-Krol G.C.M., Geraedts J.P.M., Smeets H.J.M.;  
RT "Novel KCNQ1 and HERG missense mutations in Dutch long-QT families.";  
RT Hum. Mutat. 13:301-310(1999).  
RN [12]  
RN VARIANT LQT2 ARG-572.  
RX MEDLINE-99235552; PubMed-10220146;  
RA Larsen L.A., Christiansen M., Vuust J., Andersen P.S.;  
RT "High-throughput single-strand conformation polymorphism analysis by  
RT automated capillary electrophoresis: robust multiplex analysis and  
RT pattern-based identification of allelic variants.";  
RT Hum. Mutat. 13:318-327(1999).  
RN [13]  
RN VARIANTS LQT2 L-29; T-33; R-53; Q-56; G-66; R-70; P-78 AND R-86.  
RX MEDLINE-99214568; PubMed-10187793;  
RA Chen J., Zou A., Splawski I., Keating M.T., Sanguinetti M.C.;  
RT "Long QT syndrome-associated mutations in the Per-Arnt-Sim (PAS)

RT domain of HERG potassium channels accelerate channel deactivation.";  
RT J. Biol. Chem. 274:10113-10118(1999).  
RN [14]  
RN VARIANT LQT2 LYS-629.  
RX MEDLINE-99445248; PubMed-10517660;  
RA Yoshida H., Horie M., Ohtani H., Takano M., Tsuji K., Kubota T.,  
RA Fukunami M., Sasayama S.;  
RT "Characterization of a novel missense mutation in the pore of HERG in  
RT a patient with long QT syndrome.";  
RT J. Cardiovasc. Electrophysiol. 10:1262-1270(1999).  
RN [15]  
RN VARIANT LQT2 ARG-572.  
RX MEDLINE-20197680; PubMed-10735633;  
RA Larsen L.A., Svendsen I.H., Jensen A.M., Kanters J.K., Andersen P.S.,  
RA Møller M., Sørensen S.A., Sande E., Jacobsen J.R., Vuust J.,  
RA Christiansen M.;  
RT "Long QT syndrome with a high mortality rate caused by a novel G572R  
RT missense mutation in KCNH2.";  
RT Clin. Genet. 57:125-130(2000).  
RN [16]  
RN VARIANTS LQT2.  
RX MEDLINE-20432616; PubMed-10973849;  
RA Splawski I., Shen J., Timothy K.W., Lehmann M.H., Priori S.,  
RA Robinson J.L., Moss A.J., Schwartz P.J., Towbin J.A., Vincent G.M.,  
RA Keating M.T.;  
RT "Spectrum of mutations in long-QT syndrome genes: KVLQT1, HERG, SCN5A,  
RT KCNE1, and KCNE2.";  
RT Circulation 102:1178-1185(2000).  
RN [17]  
RN FUNCTION: INWARDLY RECTIFYING CARDIAC POTASSIUM (IKr) CHANNEL.  
CC -1- SUBUNIT: MAY ASSEMBLE WITH EITHER MIRP1 OR MINK. COMPLEXES WITH  
CC MIRP1 ARE MORE STABLE.  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART.  
CC -1- DISEASE: DEFECTS IN KCNH2 ARE ASSOCIATED WITH LONG QT SYNDROME  
CC TYPE 2 (LQT2). THIS DISEASE IS CHARACTERIZED BY A PROLONGED QT  
CC SEGMENT ON THE ECG AND POLYMORPHIC VENTRICULAR ARRHYTHMIAS KNOWN  
CC AS TORSADES DE POINTES. THESE ARRHYTHMIAS OFTEN OCCUR IN RELATION  
CC TO EXERCISE OR EMOTIONAL STRESS AND MAY RESULT IN RECURRENT  
CC SYNCOPE, SEIZURES, OR SUDDEN CARDIAC DEATH. DEAFNESS IS OFTEN  
CC ASSOCIATED WITH THE SYNDROME.  
CC -1- MISCELLANEOUS: IT HAS THE ARCHITECTURAL PLAN OF THE  
CC DIPOLARIZATION-ACTIVATED POTASSIUM CHANNEL FAMILY (6 PUTATIVE  
CC TRANSMEMBRANE SEGMENTS), YET IT EXHIBITS RECTIFICATION LIKE THAT  
CC OF THE INWARD-RECTIFYING POTASSIUM CHANNELS.  
CC -1- SIMILARITY: CONTAINS 1 CYCLIC NUCLEOTIDE-BINDING DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.  
CC -1- DATABASE: NAME-LQTSdb; NOTE-KCNH2 mutations page;  
CC WWW="http://www.ssi.dk/en/forstuning/lqtsdb/herg.htm"  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL; U04270; AAA62473.1;  
DR EMBL; AB009071; BAA37096.1; JOINED.  
DR EMBL; AB009057; BAA37096.1; JOINED.  
DR EMBL; AB009058; BAA37096.1; JOINED.  
DR EMBL; AB009059; BAA37096.1; JOINED.  
DR EMBL; AB009060; BAA37096.1; JOINED.  
DR EMBL; AB009061; BAA37096.1; JOINED.  
DR EMBL; AB009062; BAA37096.1; JOINED.  
DR EMBL; AB009063; BAA37096.1; JOINED.  
DR EMBL; AB009064; BAA37096.1; JOINED.  
DR EMBL; AB009065; BAA37096.1; JOINED.  
DR EMBL; AB009066; BAA37096.1; JOINED.  
DR EMBL; AB009067; BAA37096.1; JOINED.  
DR EMBL; AB009068; BAA37096.1; JOINED.  
DR EMBL; AB009069; BAA37096.1; JOINED.  
DR EMBL; AB009070; BAA37096.1; JOINED.

DR EMBL: AJ010538; CAA09232.1; --  
 DR EMBL: AJ010539; CAA09232.1; JOINED.  
 DR EMBL: AJ010540; CAA09232.1; JOINED.  
 DR EMBL: AJ010541; CAA09232.1; JOINED.  
 DR EMBL: AJ010542; CAA09232.1; JOINED.  
 DR EMBL: AJ010543; CAA09232.1; JOINED.  
 DR EMBL: AJ010544; CAA09232.1; JOINED.  
 DR EMBL: AJ010545; CAA09232.1; JOINED.  
 DR EMBL: AJ010546; CAA09232.1; JOINED.  
 DR EMBL: AJ010547; CAA09232.1; JOINED.  
 DR EMBL: AJ010548; CAA09232.1; JOINED.  
 DR EMBL: AJ010549; CAA09232.1; JOINED.  
 DR EMBL: AJ010550; CAA09232.1; JOINED.  
 DR EMBL: AJ010551; CAA09232.1; JOINED.

## Alignment Scores:

Pred. No.:	1.44e-53	Length:	1159
Score:	1551.00	Matches:	424
Percent Similarity:	44.86%	Conservative:	143
Best Local Similarity:	33.54%	Mismatches:	337
Query Match:	25.47%	Indels:	360
DB:	1	Gaps:	38

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x HERG\_HUMAN (1-1159)

QY 1 ATGCCGGCATCGGGGCGCTCTGCGGCTCAGAACACCTCTGACACCATCGCTACG 60  
 Db 1 MetProValArgArgGlyHisValAlaProGlnSerThrPheLeuAspThrIleLeuArg 20  
 QY 61 CGCTTCACGGCAGCAGACAGTAACTGCTGCTGGGCAAGCCGCAAGTGGCGGCTCTC 120  
 Db 21 LysPheGluGlnSerArgLysPheIleLeuAlaAsnAlaArgValGluAsnGly 39  
 QY 121 CCCGTGCTACTCTGCTGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
 Db 40 AlaValIleLeuArgGlyHisValAlaProGlnSerThrPheLeuAspThrIleLeuArg 59  
 QY 181 ATGCAGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 Db 60 MetGlnArgProCysThrLysAspPheLeuIleGlyProArgThrGlnArgAlaAla 79  
 QY 241 CAACAGATCCGACAGCGCTGGACGACAGAGTTCAGGCTGAGCTGATCTGCTGCTGCT 300  
 Db 80 AlaGlnIleLeuAlaGlnAlaLeuLeuGlyAlaGlnGluArgLysValGluIleAlaPheTyr 99  
 QY 301 CGGAAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 Db 100 ArgLysAspGlySerCysPheLeuGlyValAlaValAlaProValLysAsnGluAsp 119  
 QY 361 GGGGAGGTGCTCTCTCTCTA-----GTCTCTCAGAGCATC----- 399  
 Db 120 GlyAlaValAlaIleMetPheIleLeuAsnPheGluValAlaMetGluLysAspMetValGly 139  
 QY 400 -----AGCGAAACCAAGACCGAGGGGGCCGACAGATG----- 435  
 Db 140 SerProAlaHisAspThrAsnHisArgGlyProProThrSerThrLeuAlaProGlyArg 159  
 QY 435 ----- 435  
 Db 160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgLysSer 179  
 QY 436 ---AAGGACACAGTGTGGCGCGGCGCGATATGCGCGGCG---ACGATCAAGAGCTTC 489  
 Db 180 ValArgSerGlyAlaGlyGlyAlaGlyAlaProGlyAlaValAlaValAlaValAla 199  
 QY 490 AATGCCAACCGGCG----- 503  
 Db 199 SplLeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValThrAlaMet 219  
 QY 504 -----GCGGAGCGCGGCGCTGCTCTA----- 524  
 Db 219 SpAsnHisValAlaGlyLeuGlyProAlaGlnGluArgArgAlaLeuValGlyProGlyLys 239

QY 525 ---CCACCTGTCGGGACCTGCGAAGACCCCAAGGCGAAG---CACAGTCAAT--- 576  
 Db 239 SerProArgSerAlaProGlyGlnLeuProSerProArgAlaHisSerLeuAsnPro 258  
 QY 576 ----- 576  
 Db 259 AspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgLysCysAlaSer 278  
 QY 577 -----AAGGGGTGTTTGGGAG 594  
 Db 279 ValArgArgAlaSerSerAlaAspAspIleGluAlaMetArgAlaGlyValLeuProPro 298  
 QY 595 AAACCAAC----- 603  
 Db 299 ProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsnSer 318  
 QY 603 ----- 603  
 Db 319 ThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeu 338  
 QY 603 ----- 603  
 Db 339 AsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIle 358  
 QY 603 ----- 603  
 Db 359 IleAlaProLysIleLysGlnArgThrHisAsnValThrGluLysValThrGlnValLeu 378  
 QY 604 -----TTGGCTGATGACAAAGTAAAGCGGCATCCGGAAGCGCCCTC 645  
 Db 379 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTyr 398  
 QY 646 ATCTGTGTCACGTGGGCGCATGAGACCCACCTGGATGCTGCTGCTGCTGCTGCTGCTGCT 705  
 Db 399 ThrIleLeuHisLysSerProPheLysAlaValIleAspArgThrLeuLeuLeuVal 418  
 QY 706 CTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 756  
 Db 419 IleTyrThrAlaValAlaPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGlu 438  
 QY 757 GAGCCAGTGGC-----GCCGCGCGCCGCGCAGCGTGTGACCTGGCC 801  
 Db 439 GlyProAlaThrGlnLysGlyTyrAlaCysGlnProLeuAlaValAlaAspLeuIle 458  
 QY 802 GTGAGGCTCTCTCATACCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 861  
 Db 459 ValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrValAsnAla 478  
 QY 862 TCGGCGCAGGTGTTGTTGCCCCAAAGTCCATTGGCTCCACTACGTCACACCTGCTGCT 921  
 Db 479 AsnGluGluValAlaSerHisProGlyArgGluAlaValHisTyrPheLysGlyTyrPhe 498  
 QY 922 CTGCTGATGTCATGACGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 981  
 Db 499 LeuIleAspMetValAlaAlaIleProPheAspLeuLeu----- 511  
 QY 982 TACTTCGGGCG-----CATCTGCTGAAGACGTGGCGCTGCTGCTGCTGCTGCTGCTGCT 1023  
 Db 512 IlePheGlySerGlySerGlnGluLeuIleGlyLeuLeuLysThrAlaArgLeuLeuArg 531  
 QY 1024 CTGCTGCGCGCTGCTGCGGCGGTGACCGGTACCTCGAGTACAGCGCGCGGTGCTGCTGCT 1083  
 Db 532 LeuValArgValAlaArgGlyLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeuPhe 551  
 QY 1084 CTGCTCATGCGCGCTGCTGCGGCGGTGACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143  
 Db 552 LeuLeuMetCysThrPheAlaLeuIleAlaHisIleThrLeuLysIleTyrAlaIle 571  
 QY 1144 GGCACAGCGGAGATCGACAGCAGCATTCGACCTGCTGATGCTGCTGCTGCTGCTGCTGCT 1203  
 Db 572 GlyAsnMetGluGlnProHisMetAspSer-----ArgIleGlyTyrPheHisAsn 588  
 QY 1204 CTGGCCCGCGGCTGAGACTCCCTACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263



OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila;  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91262635; PubMed=1840699;  
 RA Warme J., Drysdale R., Ganetzky B.;  
 RT "A distinct potassium channel polypeptide encoded by the Drosophila  
 eag locus.";  
 RL Science 252:1560-1562(1991).  
 CC -1- FUNCTION: PROTEIN EAG IS MOST PROBABLY A STRUCTURAL COMPONENT OF  
 THE POTASSIUM CHANNEL AND MEDIATES THE POTASSIUM PERMEABILITY OF  
 MEMBRANES.  
 CC -1- SUBUNIT: DIMER (POTENTIAL).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND  
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT  
 EVERY THIRD POSITION.  
 CC -1- MISCELLANEOUS: THE SEGMENT H5 IS THOUGHT TO LINE THE CHANNEL PORE.  
 CC -1- SIMILARITY: TO THE MEMBERS OF THE POTASSIUM CHANNEL PROTEINS  
 OF THE SH SUPERFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 CYCLIC NUCLEOTIDE-BINDING DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-STM) DIMERIZATION DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL: M61157; AAA28495.1.  
 DR PIR: A40853; A40853.  
 DR FLYBASE: FBgn0000535; eag.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR001610; PAC.  
 DR InterPro: IPR000700; PAS-assoc\_C.  
 DR InterPro: IPR000014; PAS\_domain.  
 DR Pfam: PF00027; CNMP\_binding.  
 DR Pfam: PF00520; Ion\_trans; 1.  
 DR Pfam: PF00785; PAC; 1.  
 DR SMART: SM00086; PAC; 1.  
 DR SMART: SM00091; PAS; 1.  
 DR PROSITE: PS50042; CNMP\_BINDING\_3; 1.  
 DR PROSITE: PS50112; PAS; 1.  
 DR PROSITE: PS50113; PAC; 1.  
 DR PROSITE: PS50112; PAS; 1.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Glycoprotein; Phosphorylation; Repeat.  
 FT TRANSMEM 227 246 SEGMENT S1 (POTENTIAL).  
 FT TRANSMEM 269 291 SEGMENT S2 (POTENTIAL).  
 FT TRANSMEM 314 335 SEGMENT S3 (POTENTIAL).  
 FT TRANSMEM 343 369 SEGMENT S4 (POTENTIAL).  
 FT TRANSMEM 372 393 SEGMENT S5 (POTENTIAL).  
 FT TRANSMEM 442 467 SEGMENT H5 (POTENTIAL).  
 FT TRANSMEM 471 493 SEGMENT S6 (POTENTIAL).  
 FT DOMAIN 43 97 PAS.  
 FT DOMAIN 113 165 PAC.  
 FT NP\_BIND 571 688 CNMP.  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 1174 AA; 126236 MW; 344C80DC06E4340E CRC64;

Alignment Scores:  
 Pred. No.: 2, 38e-47  
 Score: 1390.00  
 Percent Similarity: 47.57%  
 Best Local Similarity: 31.55%

Length: 1174  
 Matches: 390  
 Conservative: 198  
 Mismatches: 398

Query Match: 22.83% Indels: 250  
 DB: 1 Gaps: 42  
 US-09-965-830-1\_COPY\_6\_3257 (1-3252) x CIKE DROME (1-1174)  
 QY 1 ATGCCG---GCCATGCGGGGCGCTCTGCGCCCTCAAGACATCTCTCGACCATCGCT 57  
 DB 1 MetProGlyGlyArgArgGlyLeuValAlaProGlnAsnThrPheLeuGlnSnlleile 20  
 QY 58 ACCGCTTGACGGC---ACGACACTAACTTCGCTGGGCAAGCCGACGGGCGGG 114  
 DB 21 ArgArgSerAsnSerGlnProAspSerSerPheLeuAlaAsnAlaGlnleValasp 40  
 QY 115 CTCCTCCCGCTGCTCTACTGCTCTGATGCTTCCTGACCTCAAGGCTTCCTCCGCGCT 174  
 DB 41 ---PheProIleValTyrcysAnGlnSerPheCysGlyIleSerGlyTyrcysnArgla 59  
 QY 175 GAGTCATGACGCGGGGCTGCTGCTGCTCTCTTATGCGCAGACACGACT 228  
 DB 60 GluValMetGlnLysSerCysArgTyrcysGlyPheMetTyrcysGlyLeuThrAsp 79  
 QY 229 GAGCTCTGCGCCCAACAGATCGCAAGGCGCGGACGACGACGACGACGACGACGACG 288  
 DB 80 LysGluThrValGlyArgLeuGluThrThrLeuGlnGlnGlnGlnGlnGlnGlnGln 99  
 QY 289 CTGATCTCTGACGGAAGAGCGGGCTC----- 315  
 DB 100 IleLeuLeuTyrcysnAsnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 119  
 QY 316 -----CCGTCCTGCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATG 357  
 DB 120 AlaGlnThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 139  
 QY 358 AAAGGGAGGCGGCT 417  
 DB 140 ArgAspLeuValValLeuPheLeuLeuThrPheArgAspIleThrAlaLeuGlnGln 158  
 QY 418 GGGGCGCCCGACAGATGAGAGGAGAGAGAGTGT-----GGCGCGCGCGCGATATGCGCG 471  
 DB 159 -----ProIleAspSerGlnAspThrTyrcysGlyValLeuGlyLeuSerTyrcysAla 176  
 QY 472 ---GCAGATCCAAAGGCTTCATGCTCAACGCGCGCGAGCGCGCGCGCGCTGCTCAAC 528  
 DB 177 LeuAlaArgSerVal-----ThrArgSerArg-----Gln 186  
 QY 529 CTGTCGCGGCGACCTGACG-----AAGCAGCCCAAGGCGACGACGACGACGACGACG 582  
 DB 187 PheSerAlaHisLeuProThrLeuLysAspProThrLysGlnSerAsnLeuAlaHisMet 206  
 QY 583 GTGTTGGGGGAAACCAAACTTCGCTGAGTCAAAAGTACCGCGCATCCGAGAGTCCGCC 642  
 DB 207 MetLeuLeuSerAlaAspIleMetProGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 226  
 QY 643 TTCATCTGTTGACCTGCGGACCTAGACGACGACGACGACGACGACGACGACGACGACG 702  
 DB 227 HisLeuLeuLeuHisTyrcysAlaPheLysAlaIleThrAspTrpValIleLeuGln 246  
 QY 703 AACTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 756  
 DB 247 ThrPheTyrcysAlaIleMetValProTyrcysValAlaPheLysAsnLysThrSerGln 266  
 QY 757 GAGCCGACGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGACCTGCGGAGAGTCTCTTC 816  
 DB 267 AspLeuLeuLeu-----ValValAspSerIleValValIlePhe 281  
 QY 817 ATCTTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 876  
 DB 282 PheIleAspIleValIleLeuAsnPheHisThrPheValGlyProGlyGlyValVal 301  
 QY 877 TTGCCCCAAGTCAATTCCTTCACCTAGTCAACGACGCTGCTGCTGCTGCTGCTGCTGCT 936  
 DB 302 SerAspProLysValIleArgMetAsnTyrcysSerThrPheIleIleLeuLeu 321







Db	228	serlaaspilleuetyglymetaspmetleuvalargthargthlypheleu---	246
QY	859	AAGTCGGCCAGTGTGTGTGGCCCCAAGTCATTGGCTGCCTACAGTC--ACACAC	915
Db	247	glunginglyleumetvalmetasprlaaserhargthleutrplynhietythrglnthrleu	266
QY	916	TGGTTCCTGCTGGATGTCATGCGACGGCTGCCCTTTGACTCTGTACATGCCCTCAAGTC	975
Db	267	hispheylsleuaspvalleuSERleuValProthAspleuAlatyr---Pheylsleu	285
QY	976	AACGTGTACTTCGGGGCCCATCTGCTGAGAACGGGTGGCTGGCGCTGGCGCCCTG	1035
Db	286	glymetasTyrProglu-----LeuargPheasnargleuulysleuAlatgleu	303
QY	1036	CTTCCGGCGCTGAGCCGGATCTG-----CAGTACACG	1068
Db	304	phegluphepheasprargthrgluthrargthrasntyrProasmetpheargylegly	323
QY	1069	GGCGGTGGCTGACACCTGTCTAGCGCGGTGTGGCCCTGCTCGCGACATGGCTGCTGC	1128
Db	324	AsnleuValleuTyrilleu-----IlellelleshtrpAsnAlaCys	338
QY	1129	GTCGTGTTTACATTTGGCCAGCGGAGATCGAGACGACGAATCCGAGCTGCTGAGAT	1188
Db	339	IleTyrPheAlaIleSerLys-----PheIle	347
QY	1189	GGCTGGCTGCAGAGCTGGCGCCGCCAGCTGGAACACTCCACTACGTGtGtGGCGGAGG	1248
Db	348	GlyPhe-----	349
QY	1249	CCAGCTGGAGGGAAGCAAGCTCCGGCCAGAGTGAACACTGCAGACAGACGAGGCCAAC	1308
Db	350	-----GlythraspserrTPvalTyrProhsnValserasnProglutyrGlyArg	366
QY	1309	GGGAGGGGCTGAGAGTGTGTGGGGCGGCCCTGCTGGCGAGCGCTACATCACTCCCTC	1368
Db	367	-----LeuserarglystyrIleTyrserleu	375
QY	1369	TACTTCGCACCTCAGACGCTCACCAGCGGTGGCTTGGCAACGTGTCGCCCAACAGGAC	1428
Db	376	TyrtPserhtrleuthrleuthrThrIleGly---gluthrProProvalLysasp	394
QY	1429	ACCGAGAAGATCTTCTCCANCTGCACCATGTCAATCGGGCGCGCGGAGACGAGCGGTGGT	1488
Db	395	gluluthrleuPheValIleaspPheleuValGlyValIleuIleIlePheAlaThrIle	414
QY	1489	TTTGGGAACGTGAGGGCCATCATCAGCGCATGTAGCGCCCGCTTCTGTACACAGC	1548
Db	415	ValGlyasnValGlyserMetIleSerasnMetLsnAlaserArgAlaGluPheGlnAla	434
QY	1549	CGCACGGCGACCTGGCGGATCATATCCGATCCACCTATCCCCAAGCCCTCAAGCAG	1606
Db	435	LysIleaspserrIleLysGlnTyrMetClnPheargLysValThrLysAspleuclunhr	454
QY	1609	CGCATGCTGAGTACTTCCAGCGCACCTGGCGGTGAACAMTGCATCGACACACCGAG	1666
Db	455	ArgValIleargtrPheaspTyrleuthrPalaasnLysThrValAspLulysGlu	474
QY	1669	CTGCTGCAGACCTCCCTGCAGAGCTGCGCGACAGCATCGCCATGCACCTGCACAAAGAG	1722
Db	475	ValleuLysSerleuProaspLysleuLysAlaGluIleAlaIleasnValHisleuasp	494
QY	1729	GTCCTG---CAGCTGCCACTGTTTAGCGCGCCACCGCGGTGCTGGCGGACCTGCT	1788
Db	495	ThrleuargLysValargIlePheGlnaspCysGlnAlaGlyleuValAlaGluLeuVal	514
QY	1786	CTGAGCCCTCGCGCCGCTTCTGCAGCGCGGCGAGTACCTATCCACCAAGCGATGCC	1844
Db	515	LeuLysleuArgProAlaValPheSerProGlyaspTyrIleCysAlaLysGlyGlyIle	534
QY	1846	CTGCAGGGCCCTACTTTGTGTGCTGTGCTGCCTCAACGAGAGTGTCT---AAGGTGTC	189
Db	535	glyargglumetTyrIleIleLysgluGlyLysleuAlaValAlaGluLyspGlyIle	554

```

OY 1900 ACCGTGCTCCGACCTCCTAGGGAAGGGCGACGACTGATCGGC-----TGTGAGCTG 1947
Db 555 ThrInphenalValLeuGluYaaSpGlySerTyrPhaeGlyGluIleSerIleLeuasnIle 574
OY 1948 CCCCCGGGGGAGCAGCGTGAAGGCCCAATAGCCGACGCTGAGAGGGGCTGACGACTGCGTC 2007
Db 575 LysGlySerLysSerGlyAsnArgArgYthrAlaAsnIleArgSerIleGlyTyrSerAsp 594
OY 2008 CTGACAGTCTGTCAGCAGTCGCGCTGCACGACGACTGCGCTGATACCCGAG 2061
Db 595 LeuPheCysLeuSerLysAspAspLeuMetCglValaLeuThrGluTyrProGlu 612

RESULT 4
CNGI_RAT STANDARD; PRT; 683 AA.
CNGI_RAT 062927: 008659:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG1)
DE (Cyclic nucleotide-gated channel alpha 1) (Cyclic nucleotide-gated
DE channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)
DE (Rod photoreceptor CGMP-gated channel alpha subunit).
OS CNG1 OR CNG1L OR CNG3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Barnstable C.J., Wei J.Y.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC MEDLINE=97287732; Pubmed=9142860;
RA Ding C., Potter E.D., Qiu W., Coon S.L., Levine M.A., Guggino S.E.;
RX "Cloning and widespread distribution of the rat rod-type cyclic
RT nucleotide-gated cation channel."
RL Am. J. Physiol. 272:Cl335-Cl344(1997).
RN (3)
RP SEQUENCE OF 521-683 FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97197878; Pubmed=9045728;
RA Bradley J., Zhang Y., Bakin R., Lester H.A., Ronnett G.V., Zinn K.;
RX "Functional expression of the heteromeric 'olfactory' cyclic
RT nucleotide-gated channel in the hippocampus: a potential effector of
RT synaptic plasticity in brain neurons."
RL J. Neurosci. 17:1993-2005(1997).
CC -1- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN
CC COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN
CC BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION
CC CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD
CC PHOTORECEPTORS.
CC -1- SUBUNIT: HOMOTETRAMER OR HIGHER OLIGOMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: ROD CELLS IN THE RETINA.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation. It
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U48803; AAA92110.1; -
DR EMBL: U93851; AAC53139.1; -
DR EMBL: U76220; AAC17594.1; -
DR InterPro: IPR000636; M+channel_nlg.

```





[illegible]

BL	Nat. Genet.	19;257-259(1998).
CC	-1-	FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN COUPLED CASCADE USING CNMP AS SECOND MESSENGER. THIS PROTEIN CAN BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF CONE PHOTORECEPTORS.
CC	-1-	SUBCELLULAR LOCATION: Integral membrane protein.
CC	-1-	TISSUE SPECIFICITY: PROMINENTLY EXPRESSED IN RETINA.
CC	-1-	DISEASE: DEFECTS IN CNGA3 ARE A CAUSE OF ROD MONOCHROMACY (RMCH OR RA); ALSO KNOWN AS TOTAL COLORBLINDNESS OR ACHROMATOPSIA. RMCH IS AN AUTOSOMAL RECESSIVELY INHERITED CONDITION.
CC	-1-	SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL FAMILY.
/CC	-1-	DATABASE: NAME=Mutations of the CNGA3 gene;
/CC		NOTE=Retina International's Scientific Newsletter;
CC		MWV="http://www.retina-international.com/sci_news/cnga3mut.htm".
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way said to be modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-slb.ch/announce/or_send_an_email_to_license@isb-slb.ch).
CC		-----
DR	EMBL:	AFO65314; AAC17440.1; -
DR	EMBL:	S76069; AAD14208.1; -
DR	Genew:	HGNC:2150; CNGA3.
DR	MIM:	600053; -
DR	MIM:	216900; -
DR	InterPro:	IPR001622; K+channel_pore.
DR	InterPro:	IPR000636; M+-channel_ing.
DR	InterPro:	IPR000595; CNMP_binding.
DR	Pfam:	PF00027; CNMP_binding_1.
DR	Pfam:	PF00520; Ion_trans_1.
DR	SMART:	SMO0100; CNMP_1.
DR	PROSITE:	PS00888; CNMP_BINDING_1; 1.
DR	PROSITE:	PS00889; CNMP_BINDING_2; 1.
DR	PROSITE:	PS50042; CNMP_BINDING_3; 1.
KM	Ionic channel;	Ion transport; CAMP-binding; Transmembrane; Multigene family; Vision; Disease mutation; Polymorphism.
FT	TRANSMEM	171 192 POTENTIAL.
FT	TRANSMEM	305 325 POTENTIAL.
FT	TRANSMEM	378 397 POTENTIAL.
FT	NP_BIND	482 605 CAMP.
FT	BINDING	549 549 CAMP (POTENTIAL).
FT	BINDING	564 564 CAMP (POTENTIAL).
FT	VARIANT	153 153 T -> M.
FT	VARIANT	163 163 /FTTD-VAR_010902.
FT	VARIANT	283 283 P -> L (IN RMCH).
FT	VARIANT	283 283 /FTTD-VAR_010903.
FT	VARIANT	283 283 R -> Q (IN RMCH).
FT	VARIANT	283 283 /FTTD-VAR_010904.
FT	VARIANT	283 283 R -> W (IN RMCH).
FT	VARIANT	291 291 /FTTD-VAR_010905.
FT	VARIANT	291 291 T -> R (IN RMCH).
FT	VARIANT	410 410 /FTTD-VAR_010906.
FT	VARIANT	410 410 R -> W (IN RMCH).
FT	VARIANT	529 529 /FTTD-VAR_010910.
FT	VARIANT	529 529 V -> M (IN RMCH).
FT	VARIANT	547 547 /FTTD-VAR_010907.
FT	VARIANT	547 547 F -> L (IN RMCH).
FT	VARIANT	557 557 /FTTD-VAR_010908.
FT	VARIANT	557 557 G -> R (IN RMCH).
FT	VARIANT	557 557 /FTTD-VAR_010909.
SO	SEQUENCE	694 AA; 78838 MW; AEO0B4EE76D070A0 CRC64;
Alignment Scores:		
Pred. No.:		
Score:	4.84e-10	Length: 694
Best Local Similarity:	42.25%	Matches: 142
Percent Match:	25.31%	Conservative: 95
Query Match:	6.97%	Mismatches: 217
		Indels: 107

DB: 1 Gaps: 17

US-09-965-830-1\_COPY\_6\_3257 (1-3252) x CMG3\_HUMAN (1-694)

QY 787 GTCGTGACCTGGCCGTCGAGGTCCTTACCTGACATTTGGCTGAATTTCCGTAC 846

DB 205 ValLeuAspTyrSerAlaAspValLeuTyrValLeuAspValLeuAlaArgThr 224

QY 847 ACATTGCTGCCAAGTGGCGCAGGTGGTGTTCGCCCAAGTCCATTGGCTCCACAC 906

DB 225 GlyPheLeu---GluGlnGlyLeuMetValSerAspThrAsnArgLeuTyrGlnHis 243

QY 907 ---GTCAACACCTGCTCTCCCTGATGTCATGTCAGCGCCCTTGGACCTGCTCAT 963

DB 244 LysThrThrThrGlnPheLysLeuAspValLeuSerLeuValProThrAspLeuAlaTyr 263

QY 964 GCCTTCAAGGTCAACAGTGTACTCTGGGGCCCATCTGCTGAGACGGTGGCTGCTGCGC 1023

DB 264 ---LeuLysValGlyThrAsnTyrProGlu---ValArgPheAsnArgLeuLys 280

QY 1024 CTGCTGCGCTCTCTCCGCGCTGGACCGGTACTCG----- 1059

DB 281 PheSerArgLeuPheGlnPhePheAspArgThrGlnThrArgThrAsnTyrProAsnMet 300

QY 1060 ---CAGTACACCGCCGCTGCTGCTACACTGCTCATGGCCGCTTCCGCTGCTGCGCAC 1116

DB 301 PheArgGlnGlyAsnLeuValLeuTyrLeu-----IleIleIleHis 315

QY 1117 TGGGTGCTGCTGCTGCTTTTACATGGCGACGGGAGATCGAGACAGCAATCCGAG 1176

DB 316 ThrAsnAlaCysIleTyrPheAlaIleSerLys----- 326

QY 1177 CTGCTGAGATTGCTGCTGCTGCTGACAGCTGGCCGCGCATGAGACTCCCTACTACTG 1236

DB 327 ---PheIleGlyPhe----- 330

QY 1237 GTGGGCGGAGGCGCAGTGTGAGGAGACAGTCCGCGCAGATGCAACTGACAGCAGC 1296

DB 331 ---GlyThrAspSerTyrValTyrProAsnIleSerIlePro 343

QY 1297 AGGAGGCGCAACGGGAGCGGGCTGAGCTGTGGCGCCCGCTGCTGCGCAGCGCTAC 1336

DB 344 GlnHisGlyArg-----LeuSerArgLysTyr 352

QY 1357 ATCACTCCCTACTCTGACACTGACAGGCTCAACGAGGCGCTTCCGACAGCTCC 1416

DB 353 IleTyrSerLeuTyrTyrPheThrLeuThrLeuThrIleGly---GluThrProPro 371

QY 1417 GCCACACGCGACAGAGATCTTCCATCTGACATGTCATGCGCGCCCTGATG 1476

DB 372 ProValLysAspGlnGluTyrLeuPheValValValAspPheLeuValGlyValLeuIle 391

QY 1477 CACGCGGTGCTTTGGGAAGTGTGAGCGCATCATTCAGCGCATGTGACCGCGCTT 1536

DB 392 PheAlaThrIleValGlyAsnValGlySerMetIleSerAsnMetAlaSerArgAla 411

QY 1537 CTGTACACACGCGCGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1596

DB 412 GluPheGlnAlaLysIleAspSerIleLysGlnTyrMetGlnPheArgLysValThrLys 431

QY 1597 CCCCTAAGACGCGCATGCTGCGAGTACTTCCAGGCGCCCTGGCGCGGAGCAATGCGATC 1656

DB 432 AspLeuGlnThrArgValIleArgTyrPheAspTyrIleThrAlaAsnLysLysThrVal 451

QY 1657 GACACACGCGAGCTGCTGACGCTCCCTGAGAGCTGCGCGAGCATGCGCGCATGCGC 1716

DB 452 AspGlnLysGlnValLeuLysSerLeuProAspLysLeuLysAlaGlnIleAlaIleAsn 471

QY 1717 CTGACACAGAGGTCTG---CAGTGCACATGTTTGGAGCGCGCACCGCGCTGCTGCTG 1773

DB 472 ValHisLeuAspThrLeuLysLysValArgGlnPheGlnAspGlyGlnAlaGlyLeuLeu 491

QY 1774 CGGGCACTGTCTGTGGCCCTGCGCGCGCTTGTGACGCGCGGCGAGTACTCATTCAC 1833

DB 492 ValGlnLeuValLeuLysLeuArgProThrValPheSerProGlyAspTyrIleLysLys 511

QY 1834 CAGCGCATGCCCTGCGAGCGCCCTTACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1890

DB 512 LysGlyAspIleGlyLysGlnMetTyrIleIleAsnGlnGlyLysLeuAlaValAla 531

QY 1891 ---AAGGTGGACCGCTCTGCTGCCATCTTCAAGGAGCGCGCATGCTGCTGCTGCTG 1938

DB 532 AspAspGlyValThrGlnPheValValLeuSerAspGlySerTyrPheGlyGlnIleSer 551

QY 1939 ---TGTGAGCTGCCCCCGCGGAGAGCTGCTGAAGCCCATCCGAGCTGAGGGCTG 1995

DB 552 IleLeuAsnIleLysGlySerLysSerGlyAsnArgThrAlaAsnIleArgSerIle 571

QY 1996 AGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2055

DB 572 GlyTyrSerAspLeuPheCysLeuSerLysAspAspMetGlnAlaLeuThrGlnTyr 591

QY 2056 CCGGAGTTTGCCCGCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2115

DB 592 ProGlu----- 593

QY 2116 GCTGGGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2175

DB 594 AlaLysLysAlaLeuGlnGlnGlyArgGlnIleLeuMetLysAspAsnLeuLeuLeu 613

QY 2176 TCCACGCTGCGAGAGAGAGAGACAGATGGGAGCGGCCCGCCAGCTTCCCGACGCCCA 2235

DB 614 GluGlnLeuAlaArgAlaGlyAlaAsp-----ProLysAsp 625

QY 2236 GCTGATGAGCCCTGACGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2295

DB 626 LeuGlnGlnLysValGlnGlnLeuGlnLysSerLeuAspThrLeuGlnThrArgPheAla 645

QY 2296 AAGCTGTATCCCGCACGCTGACAGCACCC-----CGGCTGCTGCTGCTGCTGCTGCTG 2337

DB 646 ArgLeuLeuAlaGlnTyrAsnAlaThrGlnIleMetLysMetLysGlnArgLeuSerGlnLeu 665

QY 2338 -----GTTGCGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2382

DB 666 GluSerGlnValLysGlyGlyLysAspLysProLeuAlaAspGlyGlnValProGlyLys 685

QY 2383 GCT 2385

DB 686 Ala 686

RESULT 6

NCBI\_CHICK STANDARD: PRT: 735 AA.

ID Q90805;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Cyclic nucleotide gated channel, cone photoreceptor, alpha subunit (CNG channel 1) (CNG-1).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI\_TaxID=9031;

OX RN

RP SEQUENCE FROM N.A.

RX MEDLINE=93264082; PubMed=7684234;

RA Benjigk W., Altenhofen W., Mueller F., Dose A., Illing M.,

RA Mollay R.S., Kaupp U.B.;

RT "Rod and cone photoreceptor cells express distinct genes for

RT cGMP-gated channels.";

RL Neuron 10:865-877(1993).

CC -!- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN

CC COUPLED CASCADE USING cGMP AS SECOND MESSENGER. THIS PROTEIN CAN

CC BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION

CC CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF CONE



```

Db 448 tsnalaserarglaglnhghlnalnalyvalaspserrileylsglntrhethisph 468
OY 1581 CCACCGTATCCCAAGCCCTCAAGACCGCATGCTGAGTACTTCCAGGCCACTGGGC 1640
Db 468 earglysvallthlyasprenclunlarvalilelysttrpheapspyrileuttrph 488
OY 1641 GGGAACAAATGGATGCACACACCGACCTGCTGCAGAGCCCTCCGACAGAGTGGCGC 1700
Db 488 rsnlystlystrhvalaspdlulysglvalleulysasnleuprobaspysleulysal 508
OY 1701 AACACATCCGACGACCTGCACACAGAGAGTCTG---CAGCTCCACTGTTTGAAGCGGC 1757
Db 508 aculilealaleasnvalahisnaspthrleulyslyvalargllepheglnaspcy 528
OY 1758 CAGCCGCGCTGCTGCGGACCATGCTGCTGCGCCGCGCCGCTTCTGCAGCGCGG 1817
Db 528 sclunlaglyleuleuileglnleulvalleulysleulysprrthvalpbeserprogl 548
OY 1818 CGAGTACTCATCCACCAAGGCGATGCCCTGACAGCCCTCTACTTGTCTGCTGCTGCTC 1877
Db 548 yasprrthlecylystlysglyasprrleghlmetrrylleilelyseluiglyly 568
OY 1878 CATGAGAGTCTC-----AAGGCTGGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1931
Db 568 sleulalavalalaspaspdllyltherrghlnphevalValleuseraspelyserly 588
OY 1932 GATCGGC-----TGTGACTGCGCCGCGGCGGACGAGGCTGTAAGGCCAATGC 1979
Db 588 rphelyglulileserlleleuasnilleylselyserlyasnargargthral 608
OY 1980 CGAGTGAAGGGGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2039
Db 608 aasnleargserllelyltyrseraspheuphecsleuserlyaspaspelmetel 628
OY 2040 CAGCCTTGCGCTGTAACCCGAG 2061
Db 628 ualaleuthrghlurtyrproglu 635

RESULT 7
CN3_MOUSE STANDARD; PRT; 631 AA.
AC 09JUZ8; 09WV01;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 16-OCT-2001 (Rel. 40, Last sequence update)
DE Cyclic-nucleotide-gated cation channel alpha 3 (CN3 channel alpha 3)
DE (CN3-3) (CN3) (Cyclic nucleotide-gated channel alpha 3) (Cone
DE photoreceptor cGMP-gated channel alpha subunit).
GN CN3 OR CN3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Retina;
RX MEDLINE=20273944; PubMed=10813773;
RA Hirano A.A., Hack I., Maessle H., Duvoisin R.M.;
RT Cloning and immunocytochemical localization of a cyclic nucleotide-
RT gated channel alpha-subunit to all cone photoreceptors in the mouse
RT retina.
RL J. Comp. Neurol. 421:80-94(2000).
RN [2]
RP SEQUENCE OF 95-631 FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=99307448; PubMed=10377453;
RA Biel M., Seeliger M., Pfeiffer A., Kohler K., Gerstner A., Ludwig A.,
RA Jaisle G., Fauser S., Ziemer E., Hofmann F.;
RT Selective loss of cone function in mice lacking the cyclic
RT nucleotide-gated channel CN3.
RL Proc. Natl. Acad. Sci. U.S.A. 96:7553-7557(1999).
CC -1- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN

```

```

CC COUPLED CASCADE USING cGMP AS SECOND MESSENGER. THIS PROTEIN CAN
CC BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION
CC CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF CONE
CC PHOTORECEPTORS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED IN RETINA.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ243933; CAB89685.1; -
CC EMBL; AJ238239; CAB42891.1; -
CC EMBL; AJ238240; CAB42891.1; JOINED.
CC EMBL; AJ238241; CAB42891.1; JOINED.
CC MGI; MGI:1341818; CAB42891.1; JOINED.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR000636; M+channel_nlg.
CC InterPro; IPR000595; CNMP_binding.
CC Pfam; PF00020; ion_trans; 1.
CC SMART; SM01000; CNMP; 1.
CC PROSITE; PS00888; CNMP_BINDING_1; 1.
CC PROSITE; PS00889; CNMP_BINDING_2; 1.
CC PROSITE; PS00442; CNMP_BINDING_3; 1.
CC K+ Ionic channel; ion transport; CAMP-binding; Transmembrane;
CC Multigene family; Vision.
CC TRANSMEM 112 133
CC FT TRANSMEM 244 264 POTENTIAL.
CC FT TRANSMEM 320 340 POTENTIAL.
CC FT NP_BIND 423 546 CAMP.
CC FT BINDING 490 490 CAMP.
CC FT BINDING 505 505 CAMP (POTENTIAL).
CC FT BINDING 110 110 CAMP (POTENTIAL).
CC FT CONFLICT 157 157 C -> Y (IN REF. 2).
CC FT CONFLICT 157 157 L -> V (IN REF. 2).
CC SQ SEQUENCE 631 AA; 72641 MW; 4FA8CD3B9AA3FE6C CRC64;

Alignment Scores:
Pred. No.: 5.83e-10 Length: 631
Score: 422.50 Matches: 152
Percent Similarity: 43.36% Conservative: 109
Best Local Similarity: 25.25% Mismatches: 224
Query Match: 6.94% Indels: 117
DB: 1 Gaps: 22

US-09-965-830-1_COPY_6_3257 (1-3252) x CN3_MOUSE (1-631)
OY 334 GATGATACCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 393
Db 24 Aspleuasphlvalgluasnglyleuliyargvalaserargleullelserlearg 43
OY 394 -----GACATCAGCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 429
Db 44 Alatrphlaserarghlsleuhsaspelulaspelultr-----Proasp 58
OY 430 AGATGGAAGAGACAGGTGTGGCGCGCGCATATGCGCGGCGCGCATATGCGCGGCGGCTTC 489
Db 59 serpheleuasp-----Arphehlsely-----Sergluleulys 70
OY 490 AATGCAACGCGCGCGCGCGCGCGCGCGCTGCTACACACTGTCGCGGCGACCTGCAGAG 549
Db 71 GluValserThrArgLysSerAsnala----- 79
OY 550 CAGCCCAAG---GGCAAGCAACCACTCAATTAAGGGGTGTTGGGGAAGCAACCAACTTG 606
Db 80 Glmpasnpoglygluglnlysprrpaspelygluglyarglysglglu--- 98

```

OY 607 CCTGAGTAAAGTACCGCCATCCGGAAGTCCGCTTACCTGTGACGTGGGCA 666  
 Db 99 -----ProileValValAspProSerSerAsnIleTyrArgTyr 112  
 OY 667 CTGAGAGCCACCTGGATGCTTACCTGCTCGCCACACTGTATGAGCTGTACTG 726  
 Db 113 LeuThrAla-----IleAlaLeuProVal 120  
 OY 727 CCCATACAGCTGTGTGTGACACAGCAGCGAG-----CCAGTGGCC 771  
 Db 121 PheTyrAsnTrpCysLeuLeuValCysArgAlaCysPheAspGluLeuGlnSerGlnHis 140  
 OY 772 CGCGGCGCCGACGCTGTGTGACCTGCGCGCGAGAGTCTTATCCTTACATG 831  
 Db 141 LeuThrLeuTrpLeuValLeuAspPyrSerAlaAspValLeuTyrValLeuAspMetLeu 160  
 OY 832 CTGATTCCTGACACATTCCTGTCCAGTGGCGGACGAGTGTGTTCGCCAAGTCC 891  
 Db 161 ValAlaGluAlaArgThrGlyPheLeu--GluGlnGlyLeuMetValArgAspThrArg 179  
 OY 892 ATTTGGCTCCATAGTC--ACCACTGTTCCTGTGATGATCATCCAGCGTCC 948  
 Db 180 LeuTrpLysHisTyrThrLysThrLeuHisPheLysLeuAspLeuSerLeuIlePro 199  
 OY 949 TTTGACCTGCTACATGCTCTTCAAGTCAAGTGTACTGCGGCGCCATGCTGTAAGACG 1008  
 Db 200 ThrAspLeuAlaTyr--LeuLysLeuGlyValAsnTyrProGlu--LeuArgPhe 216  
 OY 1009 GTGCGCTGCTGCGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1059  
 Db 217 AsnArgLeuLeuLysPheSerArgLeuPheGluPhePheAspArgThrGluThrArgThr 236  
 OY 1060 CAGTACAGCGCGCTGTGTGTCGACACGTCATCAGCGCGTGTGCTGCTGCTGCTG 1116  
 Db 237 AsnTyrProAsnValPheArgIleGlyAsnLeuValLeuTyrThrLeuIleIleHis 256  
 OY 1117 TGGGCGCTGCTGTGTGTATTTTACATGCGCAGCGAGATCGAGACAGCATCCGAG 1176  
 Db 257 TrpAsnAlaCysIleTyrPheAlaIleSerLys----- 267  
 OY 1177 CTCTGAGATGCTGTGTGTGTCGACAGCTGCGCGCGCTGCGCTGCTGCTGCTGCTG 1236  
 Db 268 -----PheIleGlyPhe----- 271  
 OY 1237 GTGCGCGGAGCGCAGCTGAGGAGACAGCTCCGCGCAGTGCACACTGCAGCAGCAGC 1296  
 Db 272 -----GlyThrAspSerTrpValTyrProAsnThrSerLysPro 284  
 OY 1297 AGCGAGGCCAAGCGGAGCGGCTGAGCTGCTGCGCGCGCGCTGCGCGAGCGCTAC 1356  
 Db 285 GluTyrAlaArg-----LeuSerArgLysTyr 293  
 OY 1357 ATGACCTCCCTACATTCGCACTCAGCAGCTCAGCAGCTGCGCTGCGCAAGTGTCC 1416  
 Db 294 IleTyrSerLeuTyrTrpSerThrLeuThrLeuThrIleGly--GluThrProPro 312  
 OY 1417 GCCAACGAGACACGAGAGATCTTCTCCATGTGACCATGCTCATCGCGCGCTGATG 1476  
 Db 313 ProValLysAspGluLeuTyrLeuPheValValIleAspPheLeuValGlyIleIleLeu 332  
 OY 1477 CACGCGGTGTGTGTGAGCAGTGCAGCATCATCCAGCGCATGACCGCGCGCTTT 1536  
 Db 333 PheAlaThrIleValIleGlyAsnValIleGlySerMetIleSerAsnMetAsnAlaProArgVal 352  
 OY 1537 CTGTACACAGCGCAGCGCGCTGCGCGCTGCGCATCATCCGCAATCCAGTCCCAAG 1596  
 Db 353 GluPheGlnAlaLysIleAspSerValLysGlnTyrMetGlnPheArgLysValThrLys 372  
 OY 1597 CCCCTACAGCAGCGCTGCTGAGTACTTCCAGCGCCACTGCGCGCGTGAACAAGGATC 1656  
 Db 373 AspLeuGluThrArgValIleArgTrpPheAspPyrLeuTrpAlaAsnArgLysThrVal 392  
 OY 1657 GACACACAGCGCTGCTGCAAGCTCCCTCAGCAGCTGCGCGGAGACATGCGCATGAC 1716

Db 393 AspGluLysGluValLeuLysAsnLeuProAspLysLeuLysAlaGluIleAlaIleAsn 412  
 OY 1717 CTGCACACAGAGAGTCTG--CAGCTGCCACTGTTGAGCGCGCCAGCGCGCTGCTG 1773  
 Db 413 ValHisLeuAspThrLeuLysLysValArgIlePheGlnAspCysGluAlaIleLeuLeu 432  
 OY 1774 CGGCGACTGCTGTGCGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCG 1833  
 Db 433 ValGluLeuValLeuLysLeuArgProThrValPheSerProGlyAspTyrIleCysLys 452  
 OY 1834 CAGCGGATGCCCTGAGCGCGCTTACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1890  
 Db 453 LysGlyAspIleGlyArgGluMetTyrIleIleLysGluLysLeuAlaValAla 472  
 OY 1891 ---AAGGTGCGACCGCTGCTGCGCATCTTCCAGGAGCGCGCGCGCGCGCGCGCG 1938  
 Db 473 AspAspGlyValThrGlnPheValValLeuSerAspGlySerTyrPheGlyGluIleSer 492  
 OY 1939 ---TGTGACTGCG 1995  
 Db 493 IleLeuAsnIleLysGlySerLysSerGlyAsnArgArgThrAlaAsnIleArgSerIle 512  
 OY 1996 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2055  
 Db 513 GlyTyrSerAspLeuPheCysLeuSerLysAspAspLeuMetClnAlaLeuThrGluTyr 532  
 OY 2056 CCCGAG 2061  
 Db 533 ProAsp 534  
 RESULT 8  
 CNG\_DROME STANDARD; PRT; 665 AA.  
 ID CNG\_DROME 024278; 09V715;  
 AC 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DT Cyclic-nucleotide-gated cation channel (CNG channel).  
 DE CNG OR CG7779.  
 GN  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95045396; PubMed=7957070;  
 RA Baumann A., Fritts S., Godde M., Selfert R., Kaupp U.B.:  
 RT "Primary structure and functional expression of a Drosophila cyclic  
 nucleotide-gated channel present in eyes and antennae".  
 RL EMBO J. 13:5040-5050(1994).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolashkov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,  
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA She B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT Science 287:2185-2195(2000).  
 RL "The genome sequence of Drosophila melanogaster".  
 CC -1- FUNCTION: APPROXIMATELY 50-FOLD MORE SENSITIVE TO CGMP THAN TO  
 CC CAMP. MAY BE INVOLVED IN TRANSDUCTION CASCADES OF BOTH  
 CC INVERTEBRATE PHOTORECEPTORS AND OLFACTORY SENSILLAE.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ANTENNAE AND THE VISUAL SYSTEM.  
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL  
 CC FAMILY.  
 CC -----  
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, X89601; CAA61760.1; -  
 DR EMBL, AE003807; AAF58033.1; -  
 DR FLYBase, FBgn0014462; Cnq.  
 DR InterPro: IPR001622; K+channel\_pore.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR000595; CNMP\_binding.  
 DR Pfam: PF00027; CNMP\_binding; 1.  
 DR Pfam: PF00520; ion\_trans; 1.  
 DR SMART: SM00100; CNMP; 1.  
 DR PROSITE: PS00888; CNMP\_BINDING\_1; 1.  
 DR PROSITE: PS00889; CNMP\_BINDING\_2; 1.  
 DR PROSITE: PS50042; CNMP\_BINDING\_3; 1.  
 KW Ionic channel; Ion transport; CAMP-binding; Transmembrane.  
 FT DOMAIN 1 110  
 FT TRANSMEM 111 131  
 FT DOMAIN 132 138  
 FT TRANSMEM 139 159  
 FT DOMAIN 160 186  
 FT TRANSMEM 187 207  
 FT DOMAIN 208 253  
 FT TRANSMEM 254 274  
 FT DOMAIN 275 325  
 FT TRANSMEM 326 346  
 FT DOMAIN 347 481  
 FT TRANSMEM 482 502  
 FT DOMAIN 503 665  
 FT NE\_BIND 437 559  
 FT BINDING 496 511  
 FT CARBOHYD 135 135  
 FT CONFLICT 73  
 SQ SEQUENCE 665 AA; 75823 MW; 6EFC9A7CA243660 CRC64;  
 Alignment Scores:  
 Pred. No.: 6 35e-10 Length: 665  
 Score: 421.50 Matches: 155  
 Percent Similarity: 43.27% Conservative: 102

Best Local Similarity: 26.09% Mismatches: 227  
 Query Match: 6.92% Indels: 110  
 DB: 1 Gaps: 23  
 US-09-965-830-1\_COPY\_6\_3257 (1-3252) x CNG\_DROME (1-665)  
 QY 393 GGACATACAGCGAAACCAACAGAGGGGGCCCGACAGATGAGAGACAGTGGTGG 452  
 DB 20 GYGLINGNINthrasplagiupPro-----serlyasgserlys 32  
 QY 453 CCGCGCCATATAGCGCGGCGGACAGATCCAAAGGCTTCAATGCCAACCGCGCGGACCG 512  
 DB 33 ProSerAlaLeu---ArgAlrGthleuGlnAlaLeuArg---GlnrGthleuThrylsArg 50  
 QY 513 GCGCGGCTCTACACACCTCCGCGGACCTGCAGAG-----CAGCCCAAGGACAGCA 566  
 DB 51 AsnAlrGpPolysProPro-AspTrptheuGlnlyuSpheSerAsnThrThrasThras 70  
 QY 567 CAGCTCAATAGAGGGGCTTTGGGAGAAACCAACTGCGTACAGTAAAGTACCGCC 626  
 DB 70 pylsllleGlylysglyCys-----ProAlaMetGluAspAlaLeuSerSe 86  
 QY 627 CATCCGAGATGCGCCCTTCATCTGTGCATGTGGCGGACAGTACAGCC----- 675  
 DB 86 rGluIleArglygSerSerValLeu-----CysAsnAlrGleuSerValAspProThle 104  
 QY 676 -----ACCTGGAGATGCTTCATCTGCTCCGACACCTATGTGGCTGTAC 722  
 DB 104 uGlnSerHisTyrrArGtrPleuAlaIleValSerIleuAlaValLeuTyraSnlIleleph 124  
 QY 723 TGTGGCCATACAGCGTGTGTGTAGACAGACAGGAGCCAGTCCGCGCGCGCGCC 782  
 DB 124 eVal-----ValGlyArgAlaValAlrPheTrpGluIleAsnlySeraAlr 139  
 QY 783 CAGC-----GTCTGACCTGCGCGGTGAGGTCCTTCATCTTCACTTGAATGTGT 833  
 DB 139 AlaIleHetrPrrTyrrThrLeuAspTyrrLeuGlySerPheIleTyrrLeuLeuAlrPheLeuVa 159  
 QY 834 GAATTCGATACACATCTGCTGCTCCAGTCCGCGGAGGCGGTGTGGCCCAAGTCAAT 893  
 DB 159 IHISmethIsGlnGlyPheLeuAspGln---GlyLeuLeuValAlrAspAlaPheArgue 178  
 QY 894 TTGCTCCACATACGTCACACC-----TGTCTCTGTGATGTCATCAGAGCCCTGCC 947  
 DB 178 uArgAlrHisTyrrPheHisThrlyGlyTrpTyrr---LeuAspValLeuSerMetLeuPr 197  
 QY 948 CTTTACCTGCTACATGCTTC-----AAGTCAACGTGTACTTGGGGGC 992  
 DB 197 oThraspleuAlaTyrrIleTrpTrpProGluThrCysSerSerLeuTyrrLeuProCy 217  
 QY 993 CCAT---CTGTGAAGAGCGGCGCTGCTGCGCTGCTGCGCTGCTGCGCGCTGCA 1049  
 DB 217 sProValIleValAlrGlyLeuAsnAlrGlyLeuArgIleAsnAlrGlyLeuTrpGluTrpPhas 237  
 QY 1050 CCGGTACTCG-----CAGTACAGCGCGGTGCTGCTGAC 1082  
 DB 237 pairThrGlnThralrAlaThrGlyTyrrProAsnAlaPheArgIleCyslyValValLeuAl 257  
 QY 1083 ACTGCTCATGCGCGCTGCTGCGCTGCTGCGCTGCTGCGCTGCTGCTGCTGCTGCT 1142  
 DB 257 alleu-----ValleuIleHisTrpAsnAlaCysMetTyrrPheAlaI 272  
 QY 1143 TGGCCAGCGGAGATCCAGACAGCAGCAATCCGACCTGCTGAGATGGCTGCGTGCAGCA 1202  
 DB 272 eSerTyrrGluIleGlyPheSerSerAspSer-----TrpValTyrras 286  
 QY 1203 GCGGCGCGCGGATGAGAGATCCTCTACTACTGTGTGCGCGGAGCCAGCTGAGGGA 1262  
 DB 286 nLeu----- 287  
 QY 1263 CAGCTCCGCGCAGATGACAACTGACAGACAGCAGGAGCCAAAGGAGCGGCTGGA 1322  
 DB 288 -----AsnGlyThr----- 290













Db 636 HsHSTnGlyLeuengLlVleuNeuSeirspanglUaAGlUGlYcLUhISAlaGlyAlPro 655  
QY 2224 TCCCAAGCCCCAGCTGATGAGCCCTCCAGCCCC 2256  
Db 656 ThrHSTnHISAlaAsprIHISAlaGlnPro 666

RESULT 12

ID	CNG1_BOVIN	STANDARD;	PRT;	690 AA.
AC	Q00194;			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	CGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG1)			
DE	(Cyclic nucleotide-gated channel alpha 1) (Cyclic nucleotide-gated			
DE	channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)			
GN	(Rod photoreceptor CGMP-gated channel alpha subunit).			
OS	Bos taurus (Bovinae).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OX	BoVIDae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RC	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.			
RC	TISSUE-Retinal rod cell;			
RA	MEDLINE=90098076; PubMed=2481236;			
RA	Kaupp U.B., Nildome T., Tanabe T., Terada S., Boenigk W.,			
RA	Stuehmer W., Cook N.J., Kangawa K., Matsuo H., Hirose T., Miyata T.,			
RA	Numa S.;			
RT	"Primary structure and functional expression from complementary DNA			
RT	of the rod photoreceptor cyclic GMP-gated channel.";			
RL	Nature 342:762-766(1989).			
RN	[2]			
RP	3D-STRUCTURE MODELING OF 485-610.			
RP	MEDLINE=92256398; PubMed=1316156;			
RA	Kumar V.D., Weber I.T.;			
RA	"Molecular model of the cyclic GMP-binding domain of the cyclic GMP-			
RT	gated ion channel.";			
RL	Biochemistry 31:4643-4649(1992).			
RN	[3]			
RP	TOPOLOGY.			
RP	MEDLINE=95365381; PubMed=7543681;			
RA	Reim D.K., Baumann A., Kaupp U.B.;			
RT	"Probing the transmembrane topology of cyclic nucleotide-gated ion			
RT	channels with a gene fusion approach.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 92:7423-7429(1995).			
RN	[4]			
RP	TOPOLOGY.			
RP	MEDLINE=92112723; PubMed=1370452;			
RA	Wohlfiart P., Haase W., Molday R.S., Cook N.J.;			
RT	"Antibodies against synthetic peptides used to determine the topology			
RT	and site of glycosylation of the CGMP-gated channel from bovine rod			
RT	photoreceptors.";			
RL	J. Biol. Chem. 267:644-648(1992).			
CC	-1- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN			
CC	COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN			
CC	BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION			
CC	CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD			
CC	PHOTORECEPTORS.			
CC	-1- SUBUNIT: HOMOTETRAMER OR HIGHER OLIGOMER.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: ROD CELLS IN THE RETINA.			
CC	-1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL			
CC	FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-slb.ch/announce/">http://www.isb-slb.ch/announce/</a>			

```

CC      or send an email to license@lsb-sib.ch .
CC      -----
DR      EMBL: X51604; CA935947.1; -.
DR      PIR: S07103; S07103.
DR      InterPro: IPR000636; Mchannel_nlg.
DR      InterPro: IPR000595; CNMP_binding.
DR      Pfam: PF00027; CNMP_binding.1.
DR      Pfam: PF00520; ion_trans.1.
DR      SMART: SM00100; CNMP.1.
DR      PROSITE: PS00088; CNMP_BINDING_1; 1.
DR      PROSITE: PS00889; CNMP_BINDING_2; 1.
DR      PROSITE: PS50042; CNMP_BINDING_3; 1.
KW      Ionic channel, Ion transport; CNMP-binding; Transmembrane;
KW      Multigene family; Vision.
FT      DOMAIN 1 162
FT      TRANSSEM 163 183
FT      TRANSSEM 184 196
FT      TRANSSEM 197 215
FT      TRANSSEM 216 239
FT      TRANSSEM 240 259
FT      TRANSSEM 260 297
FT      TRANSSEM 298 320
FT      TRANSSEM 321 372
FT      TRANSSEM 393 476
FT      TRANSSEM 477 497
FT      TRANSSEM 498 690
FT      NP_BIND 485 607
FT      BINDING 544 559
FT      BINDING 559 559
FT      CARBOHYD 423
SQ      SEQUENCE 690 AA; 79602 MW; A01CF6567424455 CRC64;

Alignment Scores:
Pred. No.: 1,29e-09
Score: 413.50
Percent Similarity: 40.18%
Best Local Similarity: 22.37%
Query Match: 6.79%
DB: 1
Gaps: 19

US-09-965-830-1_COPY_6_3257 (1-3252) x CNGL_BOVIN (1-690)
OY 400 AGCGAACCAGAAACGAGGGGGCCCGACAGATGGAGAGACA-----GTEGTGCG 45
    |||||||
DB 52 SerGIuThrGIaSnPrOHISAlaArgAspSerPheArgSerAsnThrHisGIyseryl 71
    -CGCGCGCATATGCGCGGGGAGCATGCCAAGGTTTAATGCCACCGG 50
    |||
DB 72 GluProSerGIaArgGIuGIuThrLeuProGIuAlaIleAlaLeuPheAsnValaAsn 91
    -CGCGCGGACCGGGCCGCTCTTACCACCTGTCCGGGACCTGCAGAAAGCAGCCGAGGC 56
    92 -----SerSerAsnIuGIuGIuProIuGIu 101
OY 562 AAGCAGCGTCATTAAGGGGGGTGTGGGAGAAACCAACTTGCCTGAG----- 61
    |||
DB 102 LysIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIu 117
    -GluSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIu 117
OY 612 ----- 612
DB 118 GluAsnIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIuSIu 137
OY 613 -----TACAAAGTAGCGCGCATCGGAGAGAGTGGCCCTTCATCCCTGTG 654
    |||
DB 138 LysGIuGIuLysGIuLysAspIuSIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIu 157
    -CACGTGGGGGACACTGAAAGCCACCTGGGATGCTTCATCTGCTCGGCACATCTATGTG 714
    |||
DB 158 ProSerGIuAsnThrIuYrAsnThrPleuPheCysIleThrLeuProValaMetIuYrAsn 177
    |||
OY 715 GCTGTCACTGGGCCCTACAGCGGTGTGTGTGAGACAGACAGGAGGCCCACTGCGCGCGCG 774

```

Db 178 TrpThrMetIleAlaArgAlaGlyPheAspGluLeuGlnSerAspTyrLeuGluTyr 197  
 QY 775 GGGCCGGCCAGCGCTGTGACCTGGCCGCGAGGCTCTTCATCTGACATGTGCTG 834  
 Db 198 Trp-----LeuAlaPheAspTyrLeuSerAspValTyrLeuLeuAspMetPheVal 215  
 QY 835 AATTTCGTCACCATTCGTGTCCAAAGTCGGCCAGGTGGTGTGGCCCAAGTCATC 894  
 Db 216 ArgThrArgThrGlyTyrLeu---GluGlnIleLeuValGlyGluArgLeu 234  
 QY 895 TGCTCCACTACGTACACCACTG---TTCCTGGTGGATCTACGACGCGCTGCTT 951  
 Db 235 IleAspTyrTyrSerThrPheGlnPheLeuAspValLeuSerValIleProthr 254  
 QY 952 GACCTGTCATGCTTCAGCTCAAGCTCACTGCTGCGG-----GCCCAT 966  
 Db 255 AspleuLeuTyr-----IleLeuSerGlyTyrPantTyrProGluIleArg 269  
 QY 997 CTGCGAAGACGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1056  
 Db 270 LeuAsnArgLeuLeuArgIleSerArgMetPheGluPheGlnArgThrGluThrArg 289  
 QY 1057 TCGCAGTACAGCCGCGTGTG---CTGACACTGCTCATGCGCGTGTGCGCTGCTGCG 1113  
 Db 290 ThrAsnTyrProAsnIlePheArgIleSerAsnLeuValMetTyrIleIleIleIle 309  
 QY 1114 CACTGGGTGCGCTGCTGCTGCTTTCATGTGGCCAGCGGAGATGAGAGCAGCATCC 1173  
 Db 310 HistPheAsnAlaCysValTyrPhe----- 317  
 QY 1174 GAGCTGCTGATGATGGCTGGCTGAGAGCTGCGCCGCGCAGTGCATCTCTACTAC 1233  
 Db 317 ----- 317  
 QY 1234 CTGTGGCGCCGAGGCGACGTGAGGAGACAGCTCCGCGCAGATGACATGACAGCAGC 1293  
 Db 318 -----Ser 318  
 QY 1294 AACAGCGAGCCAGCAGCGGCGCTGAGCTGCTGGCGCCCTGCG----- 1341  
 Db 319 IleSerIleAlaIleIleIlePheGlyAsnAspThrTyrValTyrProAspValAsnAspPro 338  
 QY 1342 -----CTGCGCAGCGCTCATCACTGCTCTCTACTGCTGACACTGACAGCCTC 1389  
 Db 339 AspPheGlyArgGluAlaArgIleTyrValTyrSerLeuTyrThrPheThrLeu 358  
 QY 1390 ACCAGGTGGCGTGGCGAAGCTGCGCCAGACAGCAGCAGCAGATCTCTCATC 1449  
 Db 359 ThrThrIleIleIle---GluThrProProProValArgAspSerGluTyrPhePheVal 377  
 QY 1450 TGCACATGCTCATCGCGCGCTGATGACAGCGGTGTGGGAGAGTGCAGCGCCATC 1509  
 Db 378 AlaAspPheLeuIleGlyValIleIlePheAlaThrIleValGlyAsnIleGlySerMet 397  
 QY 1510 ATCCAGCGCATGTACGCGCGCGCTTCTTACACAGCGCGCAGCGCGCAGCTGCGGAC 1569  
 Db 398 IleSerAsnMetAsnAlaAlaArgAlaGluPheGlnAlaArgIleAspAlaIleGln 417  
 QY 1570 TACATCCGATCCACCGTATCCCAAGCCCTCAAGAGAGCGATCGGAGTACTTCAG 1629  
 Db 418 TyrMetHisPheArgAsnValSerTyrAspMetIleValIleValIleTyrPheAsp 437  
 QY 1630 GCCACCTGGCGGTGAGACATGATGACACAGCAGCGATGCTGCTCTCATC 1689  
 Db 438 TyrLeuThrPheAsnLysTyrValAspGluArgIleValLeuLysTyrLeuProAsp 457  
 QY 1690 GAGTGTGGCGAGCATGCGCATGCTGACAGAGAGTCTGT---CAGCTGCGCATG 1746  
 Db 458 LysLeuArgAlaGluIleAlaIleAsnValHisLeuAspThrLeuLysValArgIle 477  
 QY 1747 TTTGAGCGGCGCAGCGCGCTGCTGCGGCGCATGTCTGCTGCGCTGCGCGCGCTTC 1806  
 Db 478 PheAlaAspCysGluAlaGlyLeuLeuValGluLeuValLeuLysLeuGlnProGlnVal 497

QY 1807 TGCAGCGCGCGAGTACCTTCATCCACAGCGCATGCCCTGACAGCCCTCTACTTCTC 1866  
 Db 498 TyrSerProGlyAspTyrIleCysLysLysGlyAspIleGlyArgGluMetTyrIleIle 517  
 QY 1867 TGCTGTGCTCCATGAGTCTC-----AAGGTGACACCTGCTGCTGCTCATCTAGG 1920  
 Db 518 LysGluGlyLysLeuAlaValAlaAlaAspAspGlyIleThrGlnPheValValSer 537  
 QY 1921 AAGCGCACCTGATCCGCG-----TGTAGCGCGCGCGCGGAGCAGGAGTGTGA 1968  
 Db 538 AspGlySerTyrPheGlyGluIleSerIleLeuAsnIleLysGlySerLysAlaGlyAsn 557  
 QY 1969 AAGCGCAATGCGAGCATGAGAGGCGCTGACACTGCTGCTGCTGCTGCTGCTGCTGCT 2028  
 Db 558 ArgArgThrAlaAsnIleLysSerIleGlyTyrSerAspLeuPheCysLeuSerLysAsp 577  
 QY 2029 GGCCTGACAGACCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2088  
 Db 578 AspleuMetGluAlaLeuThrGluTyrProAsp-----AlaLysGlyMet 592  
 QY 2089 CGAGGAGACTGACCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2148  
 Db 593 LeuGluGluLysGlyLysGlnIleLeuMetLysAspGlyLeuLeuAspIleAsnIleAla 612  
 QY 2149 TCCCTGAGCGCGCAGACATACCTTATGCTGACGCTGAGGAGAGAGAGACA 2199  
 Db 613 AsnAlaGlySerAsp-----ProLysAspLeuGluGluLysValThr 626  
 Db 613 AsnAlaGlySerAsp-----ProLysAspLeuGluGluLysValThr 626  
 RESULT 13  
 CNG1\_HUMAN  
 ID CNG1\_HUMAN STANDARD: PRT: 686 AA.  
 AC P29973; Q16485; Q16279;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE CGMP-gated cation channel alpha 1 (CNG-1) (CNG1)  
 DE (Cyclic nucleotide-gated channel alpha 1) (cyclic nucleotide-gated  
 DE channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)  
 DE (Rod photoreceptor CGMP-gated channel alpha subunit).  
 GN CNGA1 OR CNGB1 OR CNCG.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Retina;  
 RX MEDLINE=92210603; PubMed=1372902;  
 RA Pittler S.J., Lee A.K., Altherr M.R., Howard T.A., Seldin M.F.,  
 RT Hurwitz R.L., Wasmuth J.J., Baehr W.;  
 RT "Primary structure and chromosomal localization of human and mouse  
 RT rod photoreceptor CGMP-gated cation channel.";  
 RT J. Biol. Chem. 267:6257-6262(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Retina;  
 RX MEDLINE=92356211; PubMed=1379636;  
 RA Dhallan R.S., Macke J.P., Eddy R.L., Shows T.B., Reed R.R.,  
 RT Yau K.-W., Nathans J.;  
 RT "Human rod photoreceptor CGMP-gated channel: amino acid sequence,  
 RT gene structure, and functional expression.";  
 RT J. Neurosci. 12:3248-3256(1992).  
 RN [3]  
 RP SEQUENCE OF 313-573 FROM N.A.  
 RX MEDLINE=95175019; PubMed=7532814;  
 RA Distler M., Biel M., Flockerzi V., Hofmann F.;  
 RT "Expression of cyclic nucleotide-gated cation channels in non-sensory  
 RT tissues and cells.";  
 RN Neuropharmacology 33:1275-1282(1994).  
 RN [4]  
 RP VARIANT ARP PHE-316, AND VARIANTS GLN-28 AND ASN-114.  
 RX MEDLINE=96036047; PubMed=7479749;



[illegible]



FT BINDING 513 513 CAMP (POTENTIAL).  
 FT CARBOHD 377 377 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 645 AA: 74778 MW: 989515F6IAC7D31 CRC64;  
 Alignment Scores:  
 Pred. No.: 1.62e-09 Length: 645  
 Score: 411.00 Matches: 132  
 Percent Similarity: 43.83% Conservative: 113  
 Best Local Similarity: 23.61% Mismatches: 240  
 Query Match: 6.75% Indels: 74  
 Gaps: 17  
 US-09-965-830-1\_copy\_6\_3257 (1-3252) x CNG3\_CHICK (1-645)  
 QY 547 AACGAGCCCAAGGAGGACACAGCTCAATAGGGGGTGTGGGAGAAACCAACTTG 606  
 Db 84 LysGluLysLysGluLysHsLys---AsnLys-----AspLysLysLysLys 99  
 QY 607 CCTGAGTCAAAAGTAGCCGCCATCCGGAAGTCCCTTCATCTGTGCACTGTGGGCA 666  
 Db 100 GluGluGluLys-----LysLysAspIlePheIleIleAspProIleGluLys 115  
 QY 667 CTGAGAGCCACTGGGATGGCTTATCTGCTCGCCACACTGTATGGCTGTCACTGTG 726  
 Db 116 MetTyrTyrAsnTyrPhePheCysIleThrMetProValMetTyrAsnTyrPheMetIle 135  
 QY 727 CCTACAGCCTGTGTGTAGGACGACAGCAGGAGGCCAGTCCGCCGCCGCCGCCACAC 786  
 Db 136 IleAlaAlaGluLysPheAspGluLysGlnAsnAspTyrLeuAlaValTyr-----Phe 153  
 QY 787 GTCTGTGACCTGGCCGCTGAGGAGTCTTCATCTTCATCTTCATCTTCATCTTCATCT 846  
 Db 154 IleValAspTyrValIleSerAspValIleTyrIleAlaAspMetPheValIleTyrThr 173  
 QY 847 ACATTCTGTCTCAAGTGGGCCAGGAGTGTGGTGGCCCAAGTCCATTCCTGCTCCACTAC 906  
 Db 174 GluTyrLeu---GluGlnGlyLeuLeuValLysGluGluGlnLysLysGluLysTyr 192  
 QY 907 GTCAACCAAC---TGGTCTCTCTGTGATGTATCGACGAGCTGCCCTTGTACCTGTACAT 963  
 Db 193 LysSerSerLeuGlnPheLysLeuAsnTyrProGluLeuArgIleAsnArgLeuLeuArgVal 212  
 QY 964 GCCTTCAGGTCACAGTGTG---TACTTGGGGGCCATGTGCTGAGAGAGGTCGCTGCTG 1020  
 Db 213 ---PheLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 231  
 QY 1021 CGCTGTCTGCGCTGTCTCCGCGCTGAGCTGACTGAGTGCAGTGCAGGCGCGTGTG 1077  
 Db 232 ArgMetPheGluPhePheGlnArgTyrGluTyrThrArgTyrProAsnIlePheArg 251  
 QY 1078 CTGACACTGCTCATGCGCGTGTGTGCGCTGCGCACTGCGTGCCTGCTGCTGTT 1137  
 Db 252 IleSerAsnLeuValMetTyrIleValIleIleIleHisTyrPheAsnAlaCysVal 269  
 QY 1138 TACATTGGCCAGGCGGAGATCGAGAGCAGCAATCGAGTGCCTGAGATTGCTGCTG 1197  
 Db 269 ----- 269  
 QY 1198 CAGAGACTGGCCCGCGAGTGAAGACTCCTACTACTGTGGCGCCGAGCCAGCTGGA 1257  
 Db 270 -----TyrTyrSerIleSerLysAlaIleGlyPhe 279  
 QY 1258 GGGAGACAGTCCCGCGAGTAGTGAACAATGCAAGCAGCAGCAGGAGGAGGAGG 1317  
 Db 280 GlyAlaAspThrTyrValTyrProAsnTyrSerHisPheGluPheAlaArg----- 296  
 QY 1318 CTGAGACTCTGGGCGCGCTGCGCAGGAGCTTACATCACTTCCTACTTTCGCA 1377  
 Db 297 -----LeuThrArgLysTyrValTyrSerLeuTyrTyrPse 308  
 QY 1378 CTCAGAGCTTACACAGCTGGGCTTGGCAGCAGTGTCCGCCAACAGCAGCAGAGAG 1437  
 Db 309 ThrLeuThrLeuThrThrIleGly---GluThrProProValArgAspSerGluTyr 327

QY 1438 ATCTCTCATCTGACACCATGCTCATGGGCGCCCTGATGACCGCGGTGTGTGGGAC 1497  
 Db 328 PhePheValValValAspPheLeuValGlyValLeuIlePheAlaThrIleValGlyAsn 347  
 QY 1498 GTGACGCGCCATCATCCAGCGCATGTACGCCCGCGCTTGTGTGTGTGTGTGTGTGT 1557  
 Db 348 ValGlySerMetIleSerAsnMetAsnAlaAlaArgAlaGluPheGlnAlaIleAsp 367  
 QY 1558 GACCTGCGGAGTACATCCGATCCGATCCAGTCCCAAGCGCCCTCAAGCAGCGCATGTG 1617  
 Db 368 AlaIleGlyGluTyrMetHisPheArgAsnValSerLysAspMetIleLysArgValIle 387  
 QY 1618 GAGTACTTCAGGCGCAGCTGGCGCGTGAACATGGCATGACACACACAGCTGTGCA 1677  
 Db 388 LysTyrPheAspTyrLeuTyrThrAsnLysLysAlaValAspLysLysGluValLeuLys 407  
 QY 1678 AGCTTCGCGGAGAGTGGCGGAGACATCGCATCGCATCGCATCGCATCGCATCGCATCG 1734  
 Db 408 TyrLeuProAspLysLeuArgAlaGluIleAlaIleAsnValHisIleGluThrLeuLys 427  
 QY 1735 CAGCTGCGCAGTGTGTGAGCGCGCAGCGCGGCTGCTGCGCGCATGTCTGTGCGCTG 1794  
 Db 428 LysValArgIlePheAlaAspCysGluAlaGlyLeuLeuValGluLeuValLysLysLeu 447  
 QY 1795 CGGCGCGCGCTTGTGACAGCGCGCGCGAGTCACTCATCCACAGCGAGTCCCTGCGCGC 1854  
 Db 448 GlnProGlnValTyrSerProGlyAspTyrIleCysArgGlyGlyAspIleGlyArgGlu 467  
 QY 1855 CTTCTACTTGTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1908  
 Db 468 MetTyrIleIleLysGluGlyLysLeuAlaValAlaAspAspLysValIleThrGlnPhe 487  
 QY 1909 GCCATCTAGGAGGAGGCGGACTGATCGC-----TGTGAGCTGCCCGCGCGG 1956  
 Db 488 ValValIleSerAspLysSerTyrPheGlyGluIleSerIleLeuAsnIleLysGlySer 507  
 QY 1957 GAGCAGTGTGTAAAGCGCAATGCGAGGAGGCGGAGTGTGCTGCTGCTGCTGCTGCTG 2016  
 Db 508 LysAlaGlyAsnArgArgTyrThrAlaAsnIleArgSerIleGlyTyrSerAspLeuPheCys 527  
 QY 2017 CTGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2076  
 Db 528 LeuSerLysAspAspLeuMetGlnAlaLeuThrGluTyrProAsp----- 542  
 QY 2077 AGCTGCGCTCCGAGGCGGAGCTCACTACACCTGCTGCTGCTGCTGCTGCTGCTGCTG 2136  
 Db 543 AlaLysAlaMetLeuGluGluLysGlyLysGlnIleLeuMetLysAspLysLeuLeuAsp 562  
 QY 2137 GTGACACCACTCCCTGAGCGCGGACACATACCTTATGTCCACGCTGAGAGAGAG 2193  
 Db 563 IleGluValAlaAsnLeuGlySerAsp-----ProLysAspLeuGluGluLys 578  
 RESULT 15  
 CNG2\_RABIT STANDARD: PRT; 664 AA.  
 AC Q28718;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated  
 DE cation channel 2) (CNG channel 2) (CNG-2) (Aorta CNG channel)  
 DE (RACNG).  
 GN CNG2 OR CNG2.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Aorta;  
 RX MEDLINE=93359035; PubMed=7689061;  
 RA Biel M., Altenhofen W., Hulin R., Ludwig J., Freichel M.,

[illegible]

QY	472	GCA-----	CGATCCAAAGGCTTCATTCGCAACCGGGCGGGAGC	510
Db	72	LeuValIGlyValIleArgGIInTPalalAsnApnAphArgIugIugIuaIaArgPro	91	
QY	511	CGGGCGGCGCTGTACCACTGTCGGG-----CACTGCGAG-----	AMCAGGCC	555
Db	92	AspSerPheLeuGIuaArgPheArgGlyProGIuIeugInThValThrThrlndIngly	111	
QY	556	AAGGCGACGACCAAGCTCAATATGAGGGGGGTGTGGGAGAAACCAACTGCTGAGTAC	615	
Db	112	AspGlyLys-----	GlyAspLysAspGly-----AspGly	121
QY	616	AAAGTAGCGCCGACCCGAAATGCGCCCTTCATCTGTGTGCTACTGTGGGCGACTGAGAGCC	675	
Db	122	LysGIYThrLysLysLysPheGIuLeuPheValIleuAspProAlaGlyAspTrpYrTYr	141	
QY	676	ACCTGGAGATGGCTTATCTGCTGCTGGCACACTCTATGAGGCGTGCATGTCGCTGAGCCATACAGC	735	
Db	142	ArgTrp-----	LeupheValIleAlaMetProValIleuYrAsn	154
QY	736	GTGTGTGTGACGACAGCAGCGGGAG-----CCAGTGGCGCGCGCGG-----	CCG	780
Db	155	TRPCysLeuLeuValaIaArgAlaCysPheSerAspLeuGIInArgIYrPheLeuVal	174	
QY	781	CCGAGCGTGTGTACCTGGCCCGGAGAGTGCCTTCATCTGTGACATGTGTGCGAATTC	840	
Db	175	TrpLeuValIleuAspYrPheSerAspValaTYrIleAlaAspLeuHelIeArgLeu	194	
QY	841	CGTACCAATTCGTGTCCAAAGTCCGGCCAGAGGTGTGGTGGCCCAAGTCCATTGGCTTC	900	
Db	195	ArgThrGIYpHeu-----GIuGIInGIYLeuLeuValIysAspProIysLysLeuArgAsp	213	
QY	901	CACATACATC-----ACCACTGTGTTCCTGCTGAGATGATGACGACGCTGCCCTTTGACCTG	957	
Db	214	AsnTYrIleHisThrLeuGIInPheLysLeuAspValaIaSerIleIleProThrAspLeu	233	
QY	958	CTACATGCTTCAGAGTCAAGCTCAAGCTGTACTTC-----GGGGCCCAT-----	ChGCGAG	1005
Db	234	-----	IleTYrPheAlaValaGIYIleHisAsnProGIuLeuArg	246
QY	1006	ACGGTGGCGCTGTGCGCGCTGTGCGCGCTGTCCTCCGCGGTGACGCGTACTCG-----	1059	
Db	247	PheAsnArgLeuLeuHisPheAlaArgMetPheGIuPheAspArgTrGIuThArg	266	
QY	1060	-----	CAATACAGCGCGCGTGTGTGACATGCTCATGCGCGCG	1098
Db	267	ThrSerTYrProAsnIlePheArgIleSerAsnLeuValIeuYrIleLeuValIleIle	286	
QY	1099	TTGCGCCCTGTGCGGACGACGGGTGCGCTGCTGTGTTTACATGTGGCCAGCGGAGATC	1158	
Db	287	-----	HisTrpAsnAlaCysIleTYrTYrAlaIle-----	296
QY	1159	GAGAGCAGCGCAATCCGAGCTGCCGTGAATGTGGCTGCGTACAGAGACGCGGCCGCGACTG	1218	
Db	296	-----	-----	296
QY	1219	GAGACTGCCCTACTACTGTGTGGCGCGGAGGCGACACTGGAGGAGACGCTCCGCGCAAGT	1278	
Db	296	-----	-----	296
QY	1279	GACAACTGACACAGCAGGAGCGCCACGAGCGGGGCTGAGCTGTGGGCGGCCG	1338	
Db	297	-----	SerLysSerIleGIYpHeGIYValaAspTrpIleTYrPro	310
QY	1339	TGC-----	CTGGCGAGCGCCTACATCACTCCCTCTACTTC	1374
Db	311	AsnIleThrAspProGIuTYrGIYTrLeuAlaArgIuYrIleTYrCysLeuTYrTrp	330	
QY	1375	GCACATCAAGCAGCTCAACACGCGTGGCTTCGGCAACGTGTCCGCCACACGAGACAGAG	1434	
Db	331	SerThrIleuThrIleuThrThrIleGIY-----GIuThrProProIleValIysAspGIuInu	349	
QY	1435	AAGATCTTCTCCATCTGACCATGCTATCGGGCGCCGATGACAGCGCGGTGTGGTGGG	1494	

Db 350 TyrLeuPheValIlePheAspPheLeuIleGlyValIleLeuIlePheAlaThrIleValGly 369  
QY 1495 AAGCGAGCGGCATCATCCAGCGCATGACCGCCGCGCTTCTGTACCAAGCCGACG 1554  
Db 370 AsnValGlySerMetIleSerAsnMetAsnAlaThrArgAlaGluPheGlnAlaIle 389  
QY 1555 CGCGACCTGGCGGACATCCGATCCAGCTATCCCAAGCCCTCAGACGCGCATG 1614  
Db 390 AspAlaValIleYshIstYrMetGlnPheArgIleValSerIleGlyMetGluAlaIleVal 409  
QY 1615 CTGGAGTACTTCCAGCGCACCTGGCGGTGACATGCAATGCAATGCAATGCAATGCAATG 1674  
Db 410 IleYsrTrpPheAspTrpLeuTrpThrAsnIleYsrThrValAspGluArgIleValIle 429  
QY 1675 CAGAGCTCCCTGACGAGCTGGCGGACATGCGCATGCGCATGCGCATGCGCATGCG 1734  
Db 430 LysAsnLeuProAlaIleLysLeuArgAlaGluIleAlaIleAsnValHisLeuSerThrLeu 449  
QY 1735 ---CAGTGGCACTGTTTGAGCGCGCGCGCTGCGCGCATGCTGCTGCGGC 1791  
Db 450 LysLysValArgIlePheGlnAspCysGluAlaGlyLeuLeuValGluLeuValIleLys 469  
QY 1792 CTGCGGCGCGCTTCTGACGCGCGCGGAGTACCTCATCCACCAAGCGCATGCGCTGACG 1851  
Db 470 LeuArgProGlnValPheSerProGlyAspTrpIleCysArgIleGlyAspIleGlyLys 489  
QY 1852 GCCCTTACTTGTGTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1905  
Db 490 GluMetTrpIleIleLysGluGlyLysLeuAlaValAlaAspAspGlyValThrGln 509  
QY 1906 CTGCGCATCTAGGAGGAGCGGACGTATCGGC-----TGTGAGCTGCGCGG 1953  
Db 510 TyrAlaLeuLeuSerIleGlySerCysPheGlyGluIleSerIleLeuAsnIleLysGly 529  
QY 1954 CGGAGCAGCGGTGTAAGCCCATGCGGAGCGGTGACGATGCTGCTGCTGCTGCTGCTG 2013  
Db 530 SerLysMetGlyAsnArgTrpThrAlaAsnIleArgSerLeuGlyTrpSerAspLeuPhe 549  
QY 2014 TGTGCGACGTGCTGCGCTGCGACGACGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2073  
Db 550 CysLeuSerLysAspAspLeuMetGluAlaValThrGluTrpProAspAlaIleLysVal 569  
QY 2074 TTC---AGTCGTGGC-----CTCCGAGGCGGAGCTCAGTCAACCTGGGT 2115  
Db 570 LeuGluGluArgGlyArgGluIleLeuMetLysGluGlyLeuLeuAspGluAsnGluVal 589  
QY 2116 GCTGGGAGGAGCTGCTGCGAGAGGTGACAC---AGCTCCCTGAGCGGCGACATACCTT 2172  
Db 590 Ala-----AlaSerMetGluValAspValGlnGluLysLeuLysGlnLeuGluThrAsn 607  
QY 2173 ATGTCCACGCTG----- 2184  
Db 608 MetGluThrLeuTrpThrArgPheGlyArgLeuLeuAlaGluTrpThrGlyAlaGlnGln 627  
QY 2185 -----GAGGAG 2190  
Db 628 LysLeuLysGlnArgIleThrValLeuGluValLysMetLysGlnAsnThrGluAspAsp 647  
QY 2191 AAGAGACAGATGGGAGAGCGGCGCCACGCGTCCCGGAGCGCGCATGATGAGCGCC 2247  
Db 648 TyrLeuSerAspGlyMetAsnSerPro-----GluProAlaAlaAlaGluGlnPro 664

Search completed: May 7, 2003, 15:25:14  
Job time : 95 secs

